

Gut genomics in pigs, its contribution to human health

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The gastrointestinal (GI) tract is a complex ecosystem. Interactions between food components, the cells that absorb nutrients (epithelial cells), and the permanent bacterial residents of the intestines (the micro flora) that help to digest food, are important for its proper function. Imbalance in this ecosystem may provoke the loss of the GI tract natural barrier function against pathogens and against harmful components in our diet, resulting in malfunction and consequently lead to illness.

At the Animal sciences Group (ASG) the complex interactions between the GI tract, microflora and food components are studied using the genomics technique cDNA microarrays. What microarrays actually do is measure the expression level of several thousand of genes in a biological system in a single experiment. Changes in gene expression are extrapolated to changes in expression levels of functional proteins, which in turn can be translated to biological processes. For monitoring gene expression in the GI tract of pigs ASG developed a set of probes (cDNAs) that reflects the genes expressed in the pig's intestinal epithelium, and printed them on microarray slides (object glasses). Currently, microarray slides are used that contain up to 6400 probes in quadruplicate. With this array, gene expression in the small intestine of pigs was monitored in several experimental animal models. For example, after feeding pigs with specific diets and/or feed components, and after challenging of pigs with enteric viral (rotavirus) and bacterial pathogens (*Salmonella* or enterotoxigenic *E. coli*). These experiments detected several clusters of "response genes". Among them genes whose expression are crucial for the function of the local (innate) immune defense of the pig's intestine. Particularly, our Small Intestinal Segment Perfusion (SISP) model proved to be a reliable model for monitoring gene expression in the pig's intestine (figure. 1). This SISP model allows us to generate multiple physically separated segments from the pig's intestine and separately expose these segments to different compounds or pathogens for a maximum period of 24 hours. Because up to ten segments can be applied in the pig's long small intestine many variables can be tested and analyzed by microarray analysis in a single pig. Thus, measurements in this model are isogenic, that means without natural occurring variation in gene expression between animals.

The awareness of consumers about the principle, "what you eat affects your health", has increased tremendously during the last decade. This has urged food industries to develop and produce more functional and health improving food products. Nowadays, in almost every commercial break on TV, special food products are recommended for staying healthy. Among them many products that are supplemented with biological active additives, e.g. "good" bacteria or unsaturated fatty acids. However, the mechanisms of how these special foods do their job, or in other words, how they interact with the gastrointestinal (GI) tract, are often unknown. How can genomic research in the pig's GI tract contribute to human intestinal health? Believe it or not, with respect to feed intake, digestion of feed, and its physiology, the pig resembles man. After all humans and pigs are both omnivores. Testing of (potential) biological active components of functional foods in the pig's GI tract in combination with gene expression analysis, in, for example, our SISP model may unravel the mechanism of how such food additives work. This knowledge may lead to the development of new functional foods that may improve human (intestinal) health in the future.